

5'	9	18	27	36	45	54
NCT CAG AGG CTT GTT TGC TGA GGG TGC CTG CGC AGC TGC GAC GGC TGC TGG TTT						
63	72	81	90	99	108	
TGA AAC ATG AAT CTT TCG CTC GTC CTG GCT GCC TTT TGC TTG GGA ATA GCC TCC						
M N L S L V L A A F C L G I A S						
117	126	135	144	153	162	
GCT GTT CCA AAA TTT GAC CAA AAT TTG GAT ACA AAG TGG TAC CAG TGG AAG GCA						
A V P K F D Q N L D T K W Y Q W K A						
171	180	189	198	207	216	
ACA CAC AGA AGA TTA TAT GGC GCG AAT GAA GAA GGA TGG AGG AGA GCA GTG TGG						
T H R R L Y G A N E E G W R R A V W						
225	234	243	252	261	270	
GAA AAG AAT ATG AAA ATG ATT GAA CTG CAC AAT GGG GAA TAC AGC CAA GGG AAA						
E K N M K M I E L H N G E Y S Q G K						
279	288	297	306	315	324	
CTT GGC TTC ACA ATG GCC ATG AAT GCT TTT GGT GAC ATG ACC AAT GAA GAA TTC						
L G F T M A M N A F G D M T N E E F						
333	342	351	360	369	378	
AGG CAG ATG ATG GGT TGC TTT CGA AAC CAG AAA TTC AGG AAG GGG AAA GTG TTC						
R Q M M G C F R N Q K K F R K G K V F						

FIGURE 1A

387	CGT GAG CCT CTG TTT CTT GAT CTT CCC AAA TCT GTG GAT TGG AGA AAG AAA GGC	405	414	423	432
	R E P L F L D L P K S V D W R K G				
441	TAC GTG ACG CCA GTG AAG AAT CAG AAA CAG TGT GGT TCT TGT TGG GCT TTT AGT	459	468	477	486
	Y V T P V K N Q K Q C G S C W A F S				
495	GCG ACT GGT GCT CTT GAA GGA CAG ATG TTC CGG AAA ACT GGG AAA CTT GTC TCA	513	522	531	540
	A T G A L E G Q M F R K T G K L V S				
549	CTG AGC GAG CAG AAT CTG GTG GAC TGT TCG CGT CCT CAA GGC AAT CAG GGC TGC	567	576	585	594
	L S E Q N L L V D C S R P Q G N Q G C				
603	AAT GGT GGC TTC ATG GCT AGG GCC TTC CAG TAT GTC AAC GAG AAC GGA GGC CTG	621	630	639	648
	N G G F M A R A F Q Y V K E N G G L				
657	GAC TCT GAG GAA TCC TAT CCA TAT GTA GCA GTG GAT GAA ATC TGT AAG TAC AGA	675	684	693	702
	D S E E S Y P Y V A V D E I C K Y R				

FIGURE 1B

711	720	729	738	747	756
CCT GAG AAT TCT GTT GCT AAT GAC ACT GGC TTC ACA ATG GTC GCA CCT GGA AAG					
P E N S V A A N D T G F T M V A P G K					
765	774	783	792	801	810
GAG AAG GCC CTG ATG AAA GCA GTC GCA ACT GTG GGG CCC ATC TCC GTT GCT ATG					
E K A L M K A A V A T V G P I S V A M					
819	828	837	846	855	864
GAT GCA GGC CAT TCG TCC TTC CAG TTC TAC AAA TCA GGC ATT TAT TTT GAA CCA					
D A G H S S F Q F Y K S G I Y F E P					
873	882	891	900	909	918
GAC TGC AGC AGC AAA AAC CTG GAT CAT GGT GTT CTG GTG GTT GGC TAC GGC TTT					
D C S S K N L D H G V L V G Y G F					
927	936	945	954	963	972
GAA GGA GCA AAT TCG AAT AAC AGC AAG TAT TGG CTC GTC AAA AAC AGC TGG GGT					
E G A N S N N S K Y W L V K N S W G					
981	990	999	1008	1017	1026
CCA GAA TGG GGC TCG AAT GGC TAT GTA AAA ATA GCC AAA GAC AAG AAC AAC CAC					
P E W G S N G Y V K I A K D K N N H					

FIGURE 1C

1035	1044	1053	1062	1071	1080
TGT GGA ATC GCC ACA GCA GCC AGC TAC CCC AAT GTG TGA GCT GAT GGA TGG TGA					
C G I A T A A S Y P N V					
1089	1098	1107	1116	1125	1134
GGA GGA AGG ACT TAA GGA CAG CAT GTC TGG GGA AAT TTT ATC TTG AAA CTG ACC					
1143	1152	1161	1170	1179	1188
AAA CGC TTA TTG TGT AAG ATA AAC CAG TTG AAT CAT GGA GGA TCC AAG TTG AGA					
1197	1206	1215	1224	1233	1242
TTT TAA TTC TGT GAC ATT TTT ACA AGG GTA AAA TGT TAC CAC TAC TTT AAT TAT					
1251	1260	1269	1278	1287	1296
TGT TAT ACA CAG CTT TAT GAT ATC AAA GAC TCA TTG CTT AAT TCT AAG ACT TTT					
1305	1314	1323	1332	1341	1350
GAA TTT TCA TTT TTT AAA AAG ATG TAC AAA ACA GTT TGA AAT AAA TTT TAA TTC					
1359					
GTA TAT AAA AAA AAA AA 3'					

FIGURE 1D

1 MNLSSLVLA AFCLGIA SA VPKFFDQNLDTKWYQWKATHRRLY 347021  
1 MNPTLLILA AFCLGIA SA TLTFFDHSLEAQWTKWKA MHNRLY GI 29715  
1 MKPSLLFLTA LCLGIA SA A PKLDDQNLDA DWYKWKATHGRLY GI 1468964  
  
41 GANEEGWRRRA VWEKNNMKMIELHNGEYSQGKLGFTMAMNAF 347021  
41 GMNEEGWRRRA VWEKNNMKMIELHNQ EYRE GKH SFTMAMNAF GI 29715  
41 GMNEEGWRRRA VWEKNNMKMIELHNQ EYSQGKHGF S MAMNAF GI 1468964  
  
81 GDMTNEEEFRQ MMNGFQNRKPKKGGKVFREPLFLDL PKSVDW 347021  
81 GDMTSEEEFRQ VMNGFQNRKPKKGGKVFREPLFYEA PRSVDW GI 29715  
81 GDMTNEEEFRQ VMNGFQNRKPKKGGKVFREPLVLEVPKSVDW GI 1468964  
  
121 RKKGYVTPVKNQ KQCGSCWAFS ATGAL EGGQMFRKKTGKLV S 347021  
121 REKGYVTPVKNQ GQCGSCWAFS ATGAL EGGQMFRKKTGRLLI S GI 29715  
121 REKGYVTA VKNQ GQCGSCWAFS ATGAL EGGQMFRKKTGKLV S GI 1468964  
  
161 LSEQNLVDCSRPQQGNQ GCGNGGFMARA FQYVKE NGGLDSEE 347021  
161 LSEQNLVDCSG PQGN E GCGNGGLMDYAFQYVQD NGGLDSEE GI 29715  
161 LSEQNLVDCSRPQQGNQ GCGNGGLMDN AFQYVKD NGGLDTTEE GI 1468964

FIGURE 2A

201	S	Y	P	Y	V	A	V	D	-	E	I	C	K	Y	R	P	E	N	S	V	A	N	D	T	G	F	T	M	V	A	P	G	K	E	K	A	L	M	K	A	347021
201	S	Y	P	Y	E	A	T	E	-	E	S	C	K	Y	N	P	K	Y	S	V	A	N	D	T	G	F	V	D	I	-	P	K	Q	E	K	A	L	M	K	A	GI 29715
201	S	Y	P	Y	L	G	R	E	T	N	S	C	T	Y	K	P	E	C	S	A	N	D	T	G	F	V	D	I	-	P	Q	R	E	K	A	L	M	K	A	GI 1468964	
240	V	A	T	V	G	P	I	S	V	A	M	D	A	G	H	S	S	F	Q	F	Y	K	S	G	I	Y	F	E	P	D	C	S	S	K	N	L	D	H	G	V	347021
239	V	A	T	V	G	P	I	S	V	A	I	D	A	G	H	E	S	F	L	F	Y	K	E	G	I	Y	F	E	P	D	C	S	S	E	D	M	D	H	G	V	GI 29715
240	V	A	T	V	G	P	I	S	V	A	I	D	A	G	H	S	S	F	Q	F	Y	K	S	G	I	Y	Y	D	P	D	C	S	S	K	D	L	D	H	G	V	GI 1468964
280	L	V	V	G	Y	G	F	E	G	A	N	S	N	N	S	K	Y	W	L	V	K	N	S	W	G	P	E	W	G	S	N	G	Y	V	K	I	A	K	D	K	347021
279	L	V	V	G	Y	G	F	E	S	T	E	S	D	N	N	K	Y	W	L	V	K	N	S	W	G	E	W	G	M	G	G	Y	V	K	M	A	K	D	R	GI 29715	
280	L	V	V	G	Y	G	F	E	G	T	D	S	N	S	S	K	F	W	I	V	K	N	S	W	G	P	E	W	G	W	N	G	Y	V	K	M	A	K	D	Q	GI 1468964
320	N	N	H	C	G	I	A	T	A	A	S	Y	P	N	V																										347021
319	R	N	H	C	G	I	A	S	A	A	S	Y	P	T	V																									GI 29715	
320	N	N	H	C	G	I	S	T	A	A	S	Y	P	T	V																									GI 1468964	

FIGURE 2B